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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-389-487-7.res made by jdelaval on Fri 5 Jul 102 14:17:33-PDT.


Query sequence being compared:US-09-389-487-7 (1-390)
Number of sequences searched:                  2
Number of scores above cutoff:                 2

      Results of the initial comparison of US-09-389-487-7 (1-390) with:
        File : seq5-vs-seq6.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -
N     -
C     -
E     -
S    0-----------------------------------------------------------------------
       |     |     |     |     |     |     |     |     |     |
SCORE 0     43    87    130   173   217   260   303   347   390
STDEV

                          PARAMETERS

Similarity matrix      Unitary     K-tuple                    2
Mismatch penalty             1     Joining penalty           20
Gap penalty               1.00     Window size               32
Gap size penalty          0.05
Cutoff score                 0
Randomization group          0

                       SEARCH STATISTICS

Scores:                   Mean       Median     Standard Deviation
                           390          391                   0.00

Times:                     CPU                    Total Elapsed
                    00:00:00.00                 00:00:00.00

Number of residues:                  1041
Number of sequences searched:           2
Number of scores above cutoff:          2


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

                                                                 Init. Opt.
Sequence Name     Description                          Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
   1. US-09-414-643-6 Sequence 6, Application US     390   390   390   0.00   0

A 100% similar sequence to the query sequence was found:

                                                                 Init. Opt.
Sequence Name     Description                          Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
   2. US-09-414-643-5 Sequence 5, Application US     651   390   390   0.00   0

1. US-09-389-487-7 (1-390)
   US-09-414-643-6 Sequence 6, Application US/09414643

 Sequence 6, Application US/09414643
 GENERAL INFORMATION:
  APPLICANT: PILETZ, John E.
  APPLICANT:  IVANOV, Tina R.
  TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES
  TITLE OF INVENTION:  AND POLYPEPTIDES ENCODED THEREBY
  FILE REFERENCE: Corrected Sequence Listing
  CURRENT APPLICATION NUMBER: US/09/414,643
  CURRENT FILING DATE:  1999-10-08
  PRIOR APPLICATION NUMBER: 08/922,635
  PRIOR FILING DATE: 1997-09-03
  PRIOR APPLICATION NUMBER: 60/012,600
  PRIOR FILING DATE: 1996-03-01
  NUMBER OF SEQ ID NOS: 22
  SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 6
   LENGTH: 390
   TYPE: PRT
   ORGANISM: Homo sapiens

Initial Score    =    390  Optimized Score  =    390  Significance =  0.00
Residue Identity =   100%  Matches          =    390  Mismatches   =     0
Gaps             =      0  Conservative Substitutions               =     0

    X       10        20        30        40        50        60        70
    EEEEEEDEEAEEERLALEWALGADEDFLLEHIRILKVLWCFLIHVQGSIRQFAACLVLTDFGIAVFEIPHQE
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    EEEEEEDEEAEEERLALEWALGADEDFLLEHIRILKVLWCFLIHVQGSIRQFAACLVLTDFGIAVFEIPHQE
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    SRGSSQHILSSLRFVFCFPHGDLTEFGFLMPELCLVLKVRHSENTLFIISDAANLHEFHADLRSCFAPQHMA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    SRGSSQHILSSLRFVFCFPHGDLTEFGFLMPELCLVLKVRHSENTLFIISDAANLHEFHADLRSCFAPQHMA
          80        90       100       110       120       130       140

       150       160       170       180       190       200       210
    MLCSPILYGSHTSLQEFLRQLLTFYKVAGGCQERSQGCFPVYLVYSDKRMVQTAAGDYSGNIEWASCTLCSA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    MLCSPILYGSHTSLQEFLRQLLTFYKVAGGCQERSQGCFPVYLVYSDKRMVQTAAGDYSGNIEWASCTLCSA
       150       160       170       180       190       200       210

     220       230       240       250       260       270       280
    VRRSCCAPSEAVKSAAIPYWLLLTPQHLNVIKADFNPMPNRGTHNCRNRNSFKLSRVPLSTVLLDPTRSCTQ
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    VRRSCCAPSEAVKSAAIPYWLLLTPQHLNVIKADFNPMPNRGTHNCRNRNSFKLSRVPLSTVLLDPTRSCTQ
     220       230       240       250       260       270       280

   290       300       310       320       330       340       350       360
    PRGAFADGHVLELLVGYRFVTAIFVLPHEKFHFLRVYNQLRASLQDLKTVVIAKTPGTGGSPQGSFADGQPA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    PRGAFADGHVLELLVGYRFVTAIFVLPHEKFHFLRVYNQLRASLQDLKTVVIAKTPGTGGSPQGSFADGQPA
   290       300       310       320       330       340       350       360

          370       380        X
    ERRASNDQRPQEVPAEALAPAPVEVPAPAP
    ||||||||||||||||||||||||||||||
    ERRASNDQRPQEVPAEALAPAPVEVPAPAP
          370       380       390
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